

SEQUENCE LISTING

<110> Ford, John  
Mulero, Julio

<120> METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE  
POLYPEPTIDES

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<150> 09/273,447

<151> 1999-03-19

<150> 09/118,205

<151> 1998-07-16

<150> 09/122,449

<151> 1998-07-24

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<151> 1999-02-04

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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tttgagaaaa ctctggaaca aactcctagg ggctacctca cttcctttga gatgtttaac 180

agcacttata agctctatac acatagttac ctgggatttg gattgaaagc tgcaagacta 240

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<222> (246)..(1529)

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aaaagtgata taataaagga accaaggaga aaattcagaa ggaaagaaaa aattgcctct 180
gcaggtgtgc gagcaggatt gcttctgcaa caaaagcctc caccagcca catcttgga 240
aaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta tcc 290
      Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser
        1             5             10             15

tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag 338
Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu
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Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr
              35             40             45

ttg tat gga att atg ttt gat gca ggg agc act gga act cga att cat 434
Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His
              50             55             60

gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa 482
Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu
              65             70             75

ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat 530
Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp
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caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc 578
Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala
              100             105             110

aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta 626
Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu
              115             120             125

aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct 674
Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala
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Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu	
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Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg	
180 185 190	
cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc	866
Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile	
195 200 205	
acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc	914
Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly	
210 215 220	
tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca	962
Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr	
225 230 235	
cat agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg	1010
His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu	
240 245 250 255	
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Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala	
260 265 270	
tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa	1106
Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys	
275 280 285	
tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc	1154
Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys	
290 295 300	
tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag	1202
Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu	
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gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga	1250
Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg	
320 325 330 335	
gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa	1298
Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys	
340 345 350	
gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa	1346
Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu	
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aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc 1394  
Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile  
370 375 380

aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta 1442  
Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu  
385 390 395

cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg 1490  
Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly  
400 405 410 415

gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tgaggccacg 1539  
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ttctgaacta gtctggggac atcctggact tgagcctaga gattwrgtta attaascggc 1659

cgagcttata cttwatragg taatttactt gcmtggccgc gtttacacgt cgtgatggna 1719

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<211> 428

<212> PRT

<213> Homo sapiens

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Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val  
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly  
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln  
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys  
100 105 110

Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Lys	Lys	Thr	Pro	Val	Val	Leu	Lys	115	120	125
Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Glu	His	Lys	Ala	Lys	Ala	Leu	130	135	140
Leu	Phe	Glu	Val	Lys	Glu	Ile	Phe	Arg	Lys	Ser	Pro	Phe	Leu	Val	Pro	145	150	155
Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	Leu	Ala	165	170	175
Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	Arg	Gln	180	185	190
Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr	195	200	205
Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	Gly	Tyr	210	215	220
Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	Tyr	Lys	Leu	Tyr	Thr	His	225	230	235
Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly	245	250	255
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys	260	265	270
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	275	280	285
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	290	295	300
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	305	310	315
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	325	330	335
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	340	345	350
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	355	360	365
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr	370	375	380
Ala	Leu	Leu	Lys	Asp	Gly	Phe	Gly	Phe	Ala	Asp	Ser	Thr	Val	Leu	Gln	385	390	395

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Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His  
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<211> 1287

<212> DNA

<213> Homo sapiens

<220>

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Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
20 25 30

atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg 144  
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
35 40 45

tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt 192  
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val  
50 55 60

tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg 240  
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly  
65 70 75 80

gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa 288  
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln  
85 90 95

cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa 336  
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys  
100 105 110

gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag 384  
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys  
115 120 125

gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg 432  
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu  
130 135 140

ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca	480
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro	
145 150 155 160	
aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata tta gct	528
Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala	
165 170 175	
tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga cag	576
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln	
180 185 190	
gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg	624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr	
195 200 205	
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225 230 235 240	
agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg gga	768
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly	
245 250 255	
gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt gcc tgt	816
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys	
260 265 270	
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Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr	
275 280 285	
cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat	912
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr	
290 295 300	
gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag gag	960
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu	
305 310 315 320	
gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga gct	1008
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala	
325 330 335	
gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt	1056
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val	
340 345 350	

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Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn  
355 360 365

ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc aca 1152  
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr  
370 375 380

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Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln  
385 390 395 400

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405 410 415

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<212> PRT

<213> Homo sapiens

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Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val  
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly  
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln  
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys  
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys  
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu  
130 135 140



Leu	Phe	Glu	Val	Lys	Glu	Ile	Phe	Arg	Lys	Ser	Pro	Phe	Leu	Val	Pro	145	150	155	160
Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	Leu	Ala	165	170	175	
Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	Arg	Gln	180	185	190	
Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr	195	200	205	
Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	Gly	Tyr	210	215	220	
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Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly	245	250	255	
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys	260	265	270	
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	275	280	285	
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	290	295	300	
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	305	310	315	320
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	325	330	335	
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	340	345	350	
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	355	360	365	
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr	370	375	380	
Ala	Leu	Leu	Lys	Asp	Gly	Phe	Gly	Phe	Ala	Asp	Ser	Thr	Val	Leu	Gln	385	390	395	400
Leu	Thr	Lys	Lys	Val	Asn	Asn	Ile	Glu	Thr	Gly	Trp	Ala	Leu	Gly	Ala	405	410	415	
Thr	Phe	His	Leu	Leu	Gln	Ser	Leu	Gly	Ile	Ser	His					420	425		

<211> 1287  
<212> DNA  
<213> Homo sapiens

<220>  
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atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg 144  
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
35 40 45  
  
tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt 192  
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val  
50 55 60  
  
tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg 240  
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly  
65 70 75 80  
  
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Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln  
85 90 95  
  
cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa 336  
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys  
100 105 110  
  
gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag 384  
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys  
115 120 125  
  
gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg 432  
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu  
130 135 140  
  
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Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro  
145 150 155 160  
  
aag ggc agt gtt agc atc atg act gga caa gac gaa ggc ata ttc gct 528  
Lys Gly Ser Val Ser Ile Met Thr Gly Gln Asp Glu Gly Ile Phe Ala  
165 170 175

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Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln	
180 185 190	
gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg	624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr	
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210 215 220	
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225 230 235 240	
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Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly	
245 250 255	
gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt gcc tgt	816
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys	
260 265 270	
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Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr	
275 280 285	
cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat	912
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr	
290 295 300	
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Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu	
305 310 315 320	
gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga gct	1008
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala	
325 330 335	
gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt	1056
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val	
340 345 350	
gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa aac	1104
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn	
355 360 365	
ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc aca	1152
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr	
370 375 380	
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Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln	
385 390 395 400	

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Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala  
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Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val  
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Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly  
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Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln  
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys  
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys  
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu  
130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro  
145 150 155 160

Lys Gly Ser Val Ser Ile Met Thr Gly Gln Asp Glu Gly Ile Phe Ala  
165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln  
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Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr  
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Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	Gly	Tyr	210	215	220
Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	Tyr	Lys	Leu	Tyr	Thr	His	225	230	235
Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly	245	250	255
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys	260	265	270
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	275	280	285
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	290	295	300
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	305	310	315
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	325	330	335
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	340	345	350
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	355	360	365
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr	370	375	380
Ala	Leu	Leu	Lys	Asp	Gly	Phe	Gly	Phe	Ala	Asp	Ser	Thr	Val	Leu	Gln	385	390	395
Leu	Thr	Lys	Lys	Val	Asn	Asn	Ile	Glu	Thr	Gly	Trp	Ala	Leu	Gly	Ala	405	410	415
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Val Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp  
15 20 25

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Ser Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg

                50                      55                            60

att cat gtt tac acc ttt gtg cag aaa atg cca g gtaagtgc actgggrccc 307  
Ile His Val Tyr Thr Phe Val Gln Lys Met Pro  
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atgacacatc actgcaacct tgacctcctg ggctcaagca gtccttccac ctcagcccc 607

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 Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala  
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 Ser His Trp Lys Lys Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu  
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 Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu Leu Phe Glu Val Lys  
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 Lys Thr Leu Glu Gln Xaa  
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cya trg ggc tac ctc act tcc ttt gag atg ttt aac agc act tat aag 2928  
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ctc tat aca cat ag gtgaggac ggggacaggg aagaagaata tttmwtkttg 2980  
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265 270

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295

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Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro  
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Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp  
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<223> Description of Artificial Sequence: primer

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cccaagcgaa tatgccttcg tcttgccag tcatgatgct aacactgc

48

<210> 17

<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 17  
cgaaggcata ttcgcttggg ttactgtg

28

<210> 18  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18  
cttccttcac tgggaattca gg

22

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19  
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24

<210> 20  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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29

<210> 21  
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<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer



29

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<210> 22
<211> 58
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: primer

<400> 22  
gcgctgtctc ccacagagga tcgcatcacc atcaccatca caaccagcag acttggtt 58

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<210> 23
<211> 58
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: primer

<400> 23  
aaccaagtct gctggttgtg atggtgatgg tgatgcgata ctctgtggga gacagcgc 58